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ENTERED

## RAW SEQUENCE LISTING

DATE: 04/04/2002

PATENT APPLICATION: US/09/749,728B

TIME: 14:00:07

Input Set : A:\766.43 Sequence Listing.txt

Output Set: N:\CRF3\04042002\I749728B.raw

3 <110> APPLICANT: Umezawa, Akihiro  
 4 Hata, Jun-Ichi  
 5 Fukuda, Keiichi  
 6 Ogawa, Satoshi  
 7 Sakurada, Kazuhiro  
 8 Gojo, Satoshi  
 9 Yamada, Yoji

11 <120> TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO  
 CARDIOMYOCYTES

13 <130> FILE REFERENCE: 00766.000043  
 15 <140> CURRENT APPLICATION NUMBER: US/09/749,728B  
 16 <141> CURRENT FILING DATE: 2001-09-17  
 18 <150> PRIOR APPLICATION NUMBER: H11-372826  
 19 <151> PRIOR FILING DATE: 1999-12-28  
 21 <150> PRIOR APPLICATION NUMBER: PCT-JP00-01148  
 22 <151> PRIOR FILING DATE: 2000-02-28  
 24 <150> PRIOR APPLICATION NUMBER: PCT-JP00-07741  
 25 <151> PRIOR FILING DATE: 2000-11-02  
 27 <160> NUMBER OF SEQ ID NOS: 80  
 29 <170> SOFTWARE: PatentIn Ver.2.0  
 31 <210> SEQ ID NO: 1  
 32 <211> LENGTH: 411  
 33 <212> TYPE: PRT  
 34 <213> ORGANISM: Homo sapiens

W--&gt; 35 &lt;400&gt; SEQUENCE: 1

36 Met Arg Ala His Pro Gly Gly Gly Arg Cys Cys Pro Glu Gln Glu Glu  
 37 1 5 10 15  
 38 Gly Glu Ser Ala Ala Gly Gly Ser Gly Ala Gly Gly Asp Ser Ala Ile  
 39 20 25 30  
 40 Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly  
 41 35 40 45  
 42 Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp  
 43 50 55 60  
 44 Lys Gln Ala Gly Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg  
 45 65 70 75 80  
 46 Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg  
 47 85 90 95  
 48 Pro Pro Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Cys Gly  
 49 100 105 110  
 50 Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Arg Arg Glu Pro Val Pro  
 51 115 120 125  
 52 Phe Pro Ser Gly Ser Ala Gly Pro Gly Pro Arg Gly Pro Arg Ala Thr  
 53 130 135 140  
 54 Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys

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55 145          150          155          160
56 Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp
57          165          170          175
58 Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
59          180          185          190
60 Leu Ala Arg Tyr Leu Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe
61          195          200          205
62 Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg
63          210          215          220
64 Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn
65 225          230          235          240
66 Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
67          245          250          255
68 Thr Lys Val Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
69          260          265          270
70 Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln
71          275          280          285
72 Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu
73          290          295          300
74 Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr
75 305          310          315          320
76 Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile
77          325          330          335
78 Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu
79          340          345          350
80 Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp
81          355          360          365
82 Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu
83          370          375          380
84 Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu
85 385          390          395          400
86 Met Asp Ile Glu Met Asp Ser Gly Asp Glu Ala
87          405          410

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88 &lt;210&gt; SEQ ID NO: 2

89 &lt;211&gt; LENGTH: 1233

90 &lt;212&gt; TYPE: DNA

91 &lt;213&gt; ORGANISM: Homo sapiens

W--&gt; 92 &lt;220&gt; FEATURE:

93 &lt;221&gt; NAME/KEY: CDS

94 &lt;223&gt; OTHER INFORMATION: (1)..(1236)

W--&gt; 95 &lt;400&gt; SEQUENCE: 2

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96 atg cgc gcg cac ccg ggg gga ggc cgc tgc tgc ccg gag cag gag gag 48
97 Met Arg Ala His Pro Gly Gly Gly Arg Cys Cys Pro Glu Gln Glu Glu
98 1          5          10          15
99 ggg gag agt gcg gcg ggc ggc agc ggc gct ggc ggc gac tcc gcc ata 96
100 Gly Glu Ser Ala Ala Gly Gly Ser Gly Ala Gly Gly Asp Ser Ala Ile
101          20          25          30
102 gag cag ggg ggc cag ggc agc gcg ctc gcc ccg tcc ccg gtg agc ggc 144
103 Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly

```

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104	35	40	45	
105	gtg cgc agg gaa ggc gct cgg ggc ggc ggc cgt ggc cgg ggg cgg tgg	192		
106	Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp			
107	50	55	60	
108	aag cag gcg ggc cgg ggc ggc ggc gtc tgt ggc cgt ggc cgg ggc cgg	240		
109	Lys Gln Ala Gly Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg			
110	65	70	75	80
111	ggc cgt ggc cgg gga cgg gga cgg ggc cgg ggc cgg ggc cgc ggc cgt	288		
112	Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg			
113	85	90	95	
114	ccc ccg agt ggc ggc agc ggc ctt ggc ggc gac ggc ggc ggc tgc ggc	336		
115	Pro Pro Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Cys Gly			
116	100	105	110	
117	ggc ggc ggc agc ggt ggc ggc ggc gcc ccc cgg cgg gag ccg gtc cct	384		
118	Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Arg Arg Glu Pro Val Pro			
119	115	120	125	
120	ttc ccg tcg ggg agc gcg ggg ccg ggg ccc agg gga ccc cgg gcc acg	432		
121	Phe Pro Ser Gly Ser Ala Gly Pro Gly Pro Arg Gly Pro Arg Ala Thr			
122	130	135	140	
123	gag agc ggg aag agg atg gat tgc ccg gcc ctc ccc ccc gga tgg aag	480		
124	Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys			
125	145	150	155	160
126	aag gag gaa gtg atc cga aaa tct ggg cta agt gct ggc aag agc gat	528		
127	Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp			
128	165	170	175	
129	gtc tac tac ttc agt cca agt ggt aag aag ttc aga agc aag cct cag	576		
130	Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln			
131	180	185	190	
132	ttg gca agg tac ctg gga aat act gtt gat ctc agc agt ttt gac ttc	624		
133	Leu Ala Arg Tyr Leu Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe			
134	195	200	205	
135	aga act gga aag atg atg cct agt aaa tta cag aag aac aaa cag aga	672		
136	Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg			
137	210	215	220	
138	ctg cga aac gat cct ctc aat caa aat aag ggt aaa cca gac ttg aat	720		
139	Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn			
140	225	230	235	240
141	aca aca ttg cca att aga caa aca gca tca att ttc aaa caa ccg gta	768		
142	Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val			
143	245	250	255	
144	acc aaa gtc aca aat cat cct agt aat aaa gtg aaa tca gac cca caa	816		
145	Thr Lys Val Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln			
146	260	265	270	
147	cga atg aat gaa cag cca cgt cag ctt ttc tgg gag aag agg cta caa	864		
148	Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln			
149	275	280	285	
150	gga ctt agt gca tca gat gta aca gaa caa att ata aaa acc atg gaa	912		
151	Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu			
152	290	295	300	

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153 cta ccc aaa ggt ctt caa gga gtt ggt cca ggt agc aat gat gag acc 960
154 Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr
155 305 310 315 320
156 ctt tta tct gct gtt gcc agt gct ttg cac aca agc tct gcg cca atc 1008
157 Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile
158 325 330 335
159 aca ggg caa gtc tcc gct gct gtg gaa aag aac cct gct gtt tgg ctt 1056
160 Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu
161 340 345 350
162 aac aca tct caa ccc ctc tgc aaa gct ttt att gtc aca gat gaa gac 1104
163 Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp
164 355 360 365
165 atc agg aaa cag gaa gag cga gta cag caa gta cgc aag aaa ttg gaa 1152
166 Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu
167 370 375 380
168 gaa gca ctg atg gca gac atc ttg tgc cga gct gct gat aca gaa gag 1200
169 Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu
170 385 390 395 400
171 atg gat att gaa atg gac agt gga gat gaa gcc 1233
172 Met Asp Ile Glu Met Asp Ser Gly Asp Glu Ala
173 405 410
174 <210> SEQ ID NO: 3
175 <211> LENGTH: 196
176 <212> TYPE: PRT
177 <213> ORGANISM: Homo sapiens
W--> 178 <400> SEQUENCE: 3
179 Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala
180 1 5 10 15
181 His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg
182 20 25 30
183 Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu
184 35 40 45
185 Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg
186 50 55 60
187 Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu
188 65 70 75 80
189 Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys
190 85 90 95
191 Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro
192 100 105 110
193 Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg
194 115 120 125
195 Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg
196 130 135 140
197 Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys
198 145 150 155 160
199 Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu
200 165 170 175
201 Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp

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202          180          185          190
203 Thr Asp Val Arg
204          195
205 <210> SEQ ID NO: 4
206 <211> LENGTH: 588
207 <212> TYPE: DNA
208 <213> ORGANISM: Homo sapiens
W--> 209 <220> FEATURE:
      210 <221> NAME/KEY: CDS
      211 <223> OTHER INFORMATION: (1)..(591)
W--> 212 <400> SEQUENCE: 4
213 atg agg acc ttg gct tgc ctg ctg ctc ctc ggc tgc gga tac ctc gcc 48
214 Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala
215 1 5 10 15
216 cat gtt ctg gcc gag gaa gcc gag atc ccc cgc gag gtg atc gag agg 96
217 His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg
218 20 25 30
219 ctg gcc cgc agt cag atc cac agc atc cgg gac ctc cag cga ctc ctg 144
220 Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu
221 35 40 45
222 gag ata gac tcc gta ggg agt gag gat tct ttg gac acc agc ctg aga 192
223 Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg
224 50 55 60
225 gct cac ggg gtc cac gcc act aag cat gtg ccc gag aag cgg ccc ctg 240
226 Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu
227 65 70 75 80
228 ccc att cgg agg aag aga agc atc gag gaa gct gtc ccc gct gtc tgc 288
229 Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys
230 85 90 95
231 aag acc agg acg gtc att tac gag att cct cgg agt cag gtc gac ccc 336
232 Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro
233 100 105 110
234 acg tcc gcc aac ttc ctg atc tgg ccc ccg tgc gtg gag gtg aaa cgc 384
235 Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg
236 115 120 125
237 tgc acc ggc tgc tgc aac acg agc agt gtc aag tgc cag ccc tcc cgc 432
238 Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg
239 130 135 140
240 gtc cac cac cgc agc gtc aag gtg gcc aag gtg gaa tac gtc agg aag 480
241 Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys
242 145 150 155 160
243 aag cca aaa tta aaa gaa gtc cag gtg agg tta gag gag cat ttg gag 528
244 Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu
245 165 170 175
246 tgc gcc tgc gcg acc aca agc ctg aat ccg gat tat cgg gaa gag gac 576
247 Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp
248 180 185 190
249 acg gat gtg agg 588
250 Thr Asp Val Arg

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## VERIFICATION SUMMARY

DATE: 04/04/2002

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TIME: 14:00:08

Input Set : A:\766.43 Sequence Listing.txt

Output Set: N:\CRF3\04042002\I749728B.raw

L:35 M:283 W: Missing Blank Line separator, <400> field identifier  
L:92 M:283 W: Missing Blank Line separator, <220> field identifier  
L:95 M:283 W: Missing Blank Line separator, <400> field identifier  
L:178 M:283 W: Missing Blank Line separator, <400> field identifier  
L:209 M:283 W: Missing Blank Line separator, <220> field identifier  
L:212 M:283 W: Missing Blank Line separator, <400> field identifier  
L:256 M:283 W: Missing Blank Line separator, <400> field identifier  
L:292 M:283 W: Missing Blank Line separator, <220> field identifier  
L:295 M:283 W: Missing Blank Line separator, <400> field identifier  
L:347 M:283 W: Missing Blank Line separator, <400> field identifier  
L:372 M:283 W: Missing Blank Line separator, <220> field identifier  
L:375 M:283 W: Missing Blank Line separator, <400> field identifier  
L:410 M:283 W: Missing Blank Line separator, <400> field identifier  
L:457 M:283 W: Missing Blank Line separator, <220> field identifier  
L:460 M:283 W: Missing Blank Line separator, <400> field identifier  
L:528 M:283 W: Missing Blank Line separator, <400> field identifier  
L:589 M:283 W: Missing Blank Line separator, <220> field identifier  
L:592 M:283 W: Missing Blank Line separator, <400> field identifier  
L:681 M:283 W: Missing Blank Line separator, <400> field identifier  
L:750 M:283 W: Missing Blank Line separator, <220> field identifier  
L:753 M:283 W: Missing Blank Line separator, <400> field identifier  
L:854 M:283 W: Missing Blank Line separator, <400> field identifier  
L:905 M:283 W: Missing Blank Line separator, <220> field identifier  
L:908 M:283 W: Missing Blank Line separator, <400> field identifier  
L:982 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1046 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1049 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1144 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1215 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1218 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1322 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1355 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1358 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1405 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1438 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1441 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1488 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1545 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1548 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1631 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1690 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1693 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1779 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1839 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1842 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1931 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2078 M:283 W: Missing Blank Line separator, <220> field identifier  
L:2081 M:283 W: Missing Blank Line separator, <400> field identifier

## VERIFICATION SUMMARY

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Input Set : A:\766.43 Sequence Listing.txt

Output Set: N:\CRF3\04042002\I749728B.raw

L:2270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2273 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2276 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2282 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2285 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2288 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2291 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32  
L:2299 M:283 W: Missing Blank Line separator, <220> field identifier  
L:2301 M:283 W: Missing Blank Line separator, <400> field identifier  
L:3142 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:71  
L:3153 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:72  
L:3164 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:73  
L:3175 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:74  
L:3186 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:75  
L:3197 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:76  
L:3208 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:77  
L:3219 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:78  
L:3230 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:79  
L:3241 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:80